

&lt;!--StartFragment--&gt;RESULT 1

HNL\_MANES

ID HNL\_MANES Reviewed; 258 AA.  
AC P52705;  
DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.  
DT 23-JAN-2007, sequence version 3.  
DT 24-JUL-2007, entry version 45.  
DE (S)-acetone-cyanohydrin lyase (EC 4.1.2.39) ((S)-hydroxynitrile lyase)  
DE ((S)-hydroxynitrilase) (Oxynitrilase).  
GN Name=HNL;  
OS Manihot esculenta (Cassava) (Manioc).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC rosids; eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae;  
OC Manihoteae; Manihot.  
OX NCBI\_TaxID=3983;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [MRNA], AND PROTEIN SEQUENCE OF 2-37 AND 169-192.  
RC TISSUE=Cotyledon;  
RX MEDLINE=94263231; PubMed=8203915; DOI=10.1006/abbi.1994.1267;  
RA Hughes J., Carvalho F.J.P.D.C., Hughes M.A.;  
RT "Purification, characterization, and cloning of alpha-hydroxynitrile  
RT lyase from cassava (Manihot esculenta Crantz).";  
RL Arch. Biochem. Biophys. 311:496-502(1994).  
RN [2]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
RX PubMed=11173464; DOI=10.1107/S0907444900015766;  
RA Lauble H., Foerster S., Miehllich B., Wajant H., Effenberger F.;  
RT "Structure of hydroxynitrile lyase from Manihot esculenta in complex  
RT with substrates acetone and chloroacetone: implications for the  
RT mechanism of cyanogenesis.";  
RL Acta Crystallogr. D 57:194-200(2001).  
RN [3]  
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS), AND MUTAGENESIS OF SER-80.  
RX PubMed=11316882; DOI=10.1110/ps.01301;  
RA Lauble H., Miehllich B., Foerster S., Wajant H., Effenberger F.;  
RT "Mechanistic aspects of cyanogenesis from active-site mutant Ser80Ala  
RT of hydroxynitrile lyase from Manihot esculenta in complex with acetone  
RT cyanohydrin.";  
RL Protein Sci. 10:1015-1022(2001).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).  
RX PubMed=11742123; DOI=10.1110/ps.ps.33702;  
RA Lauble H., Miehllich B., Foerster S., Kobler C., Wajant H.,  
RA Effenberger F.;  
RT "Structure determinants of substrate specificity of hydroxynitrile  
RT lyase from Manihot esculenta.";  
RL Protein Sci. 11:65-71(2002).  
CC -!- FUNCTION: Involved in cyanogenesis, the release of HCN from

CC injured tissues. Decomposes a varieties of (R) or (S) cyanohydrins  
 CC into HCN and the corresponding aldehydes and ketones. The natural  
 CC substrate of this enzyme is (S)-acetone cyanohydrin.  
 CC -!- CATALYTIC ACTIVITY: 2-hydroxyisobutyronitrile = cyanide + acetone.  
 CC -!- SUBUNIT: Homotrimer.  
 CC -!- SIMILARITY: Belongs to the AB hydrolase superfamily.  
 CC Hydroxynitrile lyase family.  
 CC -----  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC -----  
 DR EMBL; Z29091; CAA82334.1; -; mRNA.  
 DR PDB; 1DWO; X-ray; A/B=1-258.  
 DR PDB; 1DWP; X-ray; A/B=1-258.  
 DR PDB; 1DWQ; X-ray; A/B=1-258.  
 DR PDB; 1E89; X-ray; A/B=1-258.  
 DR PDB; 1E8D; X-ray; A/B=1-258.  
 DR PDB; 1EB8; X-ray; A/B=1-258.  
 DR PDB; 1EB9; X-ray; A/B=1-258.  
 DR BioCyc; MetaCyc:MONOMER-6902; -.  
 DR GO; GO:0046991; F:hydroxynitrilase activity; IEA:EC.  
 DR InterPro; IPR000073; AB\_hydrolase\_1.  
 DR Pfam; PF00561; Abhydrolase\_1; 1.  
 PE 1: Evidence at protein level;  
 KW 3D-structure; Direct protein sequencing; Lyase.  
 FT INIT\_MET 1 1 Removed.  
 FT CHAIN 2 258 (S)-acetone-cyanohydrin lyase.  
 FT /FTId=PRO\_0000084018.  
 FT ACT\_SITE 80 80 By similarity.  
 FT ACT\_SITE 208 208 By similarity.  
 FT ACT\_SITE 236 236 By similarity.  
 FT MUTAGEN 80 80 S->A: Loss of activity.  
 FT STRAND 4 8  
 FT HELIX 15 18  
 FT HELIX 21 27  
 FT STRAND 31 35  
 FT HELIX 47 49  
 FT HELIX 53 56  
 FT HELIX 58 66  
 FT STRAND 73 79  
 FT HELIX 82 92  
 FT HELIX 93 95  
 FT STRAND 96 104  
 FT STRAND 109 111  
 FT HELIX 115 123  
 FT STRAND 131 136  
 FT STRAND 142 147  
 FT HELIX 150 156  
 FT HELIX 163 172

FT	HELIX	180	184
FT	TURN	191	193
FT	HELIX	194	196
FT	STRAND	197	203
FT	STRAND	208	210
FT	HELIX	212	221
FT	STRAND	225	229
FT	HELIX	237	240
FT	HELIX	242	256
SQ	SEQUENCE	258 AA;	29372 MW; 98ABA050AC8AF1C5 CRC64;

Query Match 100.0%; Score 1360; DB 1; Length 258;  
Best Local Similarity 100.0%; Pred. No. 9.1e-102;  
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MVTAHFVLIHTICHGAWIWHKLKPALERAGHKVTALDMAASGIDPRQIEQINSFDEYSEP	60
Db	1	MVTAHFVLIHTICHGAWIWHKLKPALERAGHKVTALDMAASGIDPRQIEQINSFDEYSEP	60
Qy	61	LLTFLEKLPQGEKVIIVGES CAGLNIAIAADRYVDKIAAGVFHNSLLPDTVHSPSYTVEK	120
Db	61	LLTFLEKLPQGEKVIIVGES CAGLNIAIAADRYVDKIAAGVFHNSLLPDTVHSPSYTVEK	120
Qy	121	LLESFPDWRDTEYFTFTNITGETITTMKLG FVLLRENLF TKCTDGEYELAKMVMRKGS LF	180
Db	121	LLESFPDWRDTEYFTFTNITGETITTMKLG FVLLRENLF TKCTDGEYELAKMVMRKGS LF	180
Qy	181	QNVLAQRPKFTEKGYGSIKKVYI WTDQDKIFLPDFQRWQ IANYKPDKVYQVQGGDHKLQL	240
Db	181	QNVLAQRPKFTEKGYGSIKKVYI WTDQDKIFLPDFQRWQ IANYKPDKVYQVQGGDHKLQL	240
Qy	241	TKTEEVAHILQE VADAYA	258
Db	241	TKTEEVAHILQE VADAYA	258

<!--EndFragment-->